

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 4, 2004, 20:02:20 ; Search time 8051 Seconds
(without alignments)
2756.382 Million cell updates/sec

Title: US-09-743-209A-2
Perfect score: 2618
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09743209/runat_02062004_111815_22096/app_query.fasta_1.711

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09743209_@CGN_1_1_7406_@runat_02062004_111815_22096 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2618	100.0	1542	1	AF071051-GB 8/15/98	AF071051 Streptomy
2	2618	100.0	1542	6	AR151707 USP 6232106	AR151707 Sequence
3	2618	100.0	1542	6	AR352528 6589775	AR352528 Sequence
4	2618	100.0	1542	6	AX006515 WO 00/03581	AX006515 Sequence Appl.
5	2618	100.0	1542	6	BD217691 JP 2002520033	BD217691 Process f
6	2618	100.0	11604	6	AR151704	AR151704 Sequence
7	2618	100.0	11604	6	AR352525	AR352525 Sequence
8	2618	100.0	15079	6	AR151702	AR151702 Sequence
9	2618	100.0	15120	1	SCU87786-GB 3/6/98	U87786 Streptomyce
10	2618	100.0	15120	6	AR352523	AR352523 Sequence
11	2618	100.0	29870	6	AX763606 WO 03/040372	AX763606 Sequence
12	2229	85.1	6584	1	SCPAHCAS	GB-X84101 S.clavulige-fragment
c 13	1051	40.1	5945	1	AY426768	AY426768 Streptomy
c 14	420.5	16.1	32329	1	SCA421798	AJ421798 Streptomy
c 15	363	13.9	10481	1	AE013530	AE013530 Methanosa
16	348	13.3	10029	1	AE010880	AE010880 Methanosa

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 4, 2004, 18:56:39 ; Search time 748 Seconds
(without alignments)
2907.858 Million cell updates/sec

Title: US-09-743-209A-2
Perfect score: 2618
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09743209/runat_02062004_111815_22059/app_query.fasta_1
.711

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09743209_@CGN_1_1_885_@runat_02062004_111815_22059 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*.
1: geneseqn1980s:*.
2: geneseqn1990s:*.
3: geneseqn2000s:*.
4: geneseqn2001as:*.
5: geneseqn2001bs:*.
6: geneseqn2002s:*.
7: geneseqn2003as:*.
8: geneseqn2003bs:*.
9: geneseqn2003cs:*.
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2618	100.0	1542	3	AAZ60717	Aaz60717 DNA encod
2	2618	100.0	1542	4	AAD14504	Aad14504 S. clavul
3	2618	100.0	1542	7	ACA62927	Aca62927 DNA encod
4	2618	100.0	1542	9	ADD26445	Add26445 Streptomy
5	2618	100.0	11604	4	AAD14501	Aad14501 Streptomy
6	2618	100.0	11604	7	ACA62924	Aca62924 Clavulani
7	2618	100.0	11604	9	ADD26442	Add26442 Streptomy
8	2618	100.0	15079	2	AAQ91580	Aaq91580 S. clavul
9	2618	100.0	15079	4	AAD14499	Aad14499 Streptomy
10	2618	100.0	15079	7	ACA62922	Aca62922 Streptomy
11	2618	100.0	15120	9	ADD26455	Add26455 Streptomy
12	2618	100.0	29870	7	AAD36874	Aad36874 Streptomy
13	330	12.6	8341	2	AAT09700	Aat09700 DNA encod
14	274	10.5	1956	7	ACA38291	Aca38291 Prokaryot
c 15	273.5	10.4	40138	2	AAV81946	Aav81946 V. marinu
c 16	273.5	10.4	40138	3	AAA71520	Aaa71520 V. marinu
c 17	273.5	10.4	41587	4	AAI64984	Aai64984 Moritella
18	271	10.4	1959	7	ACA40616	Aca40616 Prokaryot
19	271	10.4	110000	4	AAI99682_24	Continuation (25 o
20	271	10.4	110000	4	AAI99683_24	Continuation (25 o
21	265.5	10.1	1770	7	ACA42428	Aca42428 Prokaryot
22	263	10.0	1506	7	ACF70233	Acf70233 Photorhab
c 23	263	10.0	110000	7	ACF65385_3	Continuation (4 of
c 24	263	10.0	110000	7	ACF65385_4	Continuation (5 of
c 25	263	10.0	110000	7	ACF67367_33	Continuation (34 o
26	258	9.9	1929	7	ACA37874	Aca37874 Prokaryot
27	257.5	9.8	1866	7	ACA26323	Aca26323 Prokaryot
28	251.5	9.6	1863	7	ABT32130	Abt32130 Benzodiaz
c 29	251.5	9.6	32539	7	ABT32129	Abt32129 Benzodiaz
30	245.5	9.4	1773	7	ADA71087	Ada71087 Rice gene
31	238.5	9.1	58857	3	AAA58471	Aaa58471 Nucleotid
32	237	9.1	1803	7	ACA37755	Aca37755 Prokaryot
33	237	9.1	1962	7	ACA23550	Aca23550 Prokaryot
34	235	9.0	1533	7	ACF67631	Acf67631 Photorhab
c 35	235	9.0	110000	7	ACF65383_1	Continuation (2 of
c 36	235	9.0	110000	7	ACF67367_02	Continuation (3 of
37	233	8.9	1665	7	ACA51672	Aca51672 Prokaryot
38	232.5	8.9	1836	3	AAC46946	Aac46946 Arabidops
39	232	8.9	1665	7	ACA32421	Aca32421 Prokaryot
40	231	8.8	1959	7	ACA26531	Aca26531 Prokaryot
41	229.5	8.8	1872	4	AAF77894	Aaf77894 Quorum se
42	229.5	8.8	2034	7	ACA39722	Aca39722 Prokaryot
43	227	8.7	1662	7	ACA35379	Aca35379 Prokaryot
44	227	8.7	1788	7	ACA45735	Aca45735 Prokaryot
c 45	226	8.6	30001	2	AAT61016	Aat61016 Total DNA

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 4, 2004, 14:00:59 ; Search time 119 Seconds
(without alignments)
2387.688 Million cell updates/sec

Title: US-09-743-209A-2
Perfect score: 2618
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRRTARGAA 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-

Q=/cgn2_1/USPTO_spool_p/US09743209/runat_02062004_111813_21989/app_query.fasta_1
.711
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09743209 @CGN_1_1_128 @runat_02062004_111813_21989 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	2618	100.0	1542	3	US-09-385-028-16✓	Sequence 16, Appl
	2	2618	100.0	1542	4	US-09-726-614-16✓	Sequence 16, Appl
	3	2618	100.0	1542	4	US-09-385-040-16✓	Sequence 16, Appl
	4	2618	100.0	11604	3	US-09-385-028-13	Sequence 13, Appl
	5	2618	100.0	11604	4	US-09-726-614-13	Sequence 13, Appl
	6	2618	100.0	11604	4	US-09-385-040-13	Sequence 13, Appl
	7	2618	100.0	15079	3	US-09-385-028-1	Sequence 1, Appli
	8	2618	100.0	15079	4	US-09-726-614-1	Sequence 1, Appli
	9	2618	100.0	15120	4	US-09-385-040-1	Sequence 1, Appli
	10	330	12.6	8341	2	US-08-737-825-1	Sequence 1, Appli
c	11	273.5	10.4	40138	3	US-09-090-793-12	Sequence 12, Appl
c	12	273.5	10.4	40138	4	US-09-231-899-12	Sequence 12, Appl
	13	271	10.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	14	271	10.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	15	265.5	10.1	1944	4	US-09-252-991A-889	Sequence 889, App
	16	236	9.0	2067	4	US-09-252-991A-16177	Sequence 16177, A
c	17	226	8.6	30001	1	US-08-125-468-1	Sequence 1, Appli
c	18	226	8.6	30001	2	US-08-474-933-1	Sequence 1, Appli
	19	209.5	8.0	1635	4	US-09-489-039A-5962	Sequence 5962, Ap
	20	209	8.0	1920	4	US-09-252-991A-8518	Sequence 8518, Ap
c	21	204.5	7.8	2013	4	US-09-252-991A-8359	Sequence 8359, Ap
	22	204.5	7.8	2409	4	US-09-252-991A-8479	Sequence 8479, Ap
	23	203	7.8	2002	6	5256558-3	Patent No. 5256558
	24	188.5	7.2	1886	6	5256558-1	Patent No. 5256558
	25	187	7.1	1992	4	US-09-220-132-55	Sequence 55, Appl
c	26	186	7.1	1368	4	US-09-252-991A-1071	Sequence 1071, Ap
	27	174	6.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	28	171.5	6.6	43280	2	US-08-804-227C-1	Sequence 1, Appli
	29	170	6.5	33529	3	US-09-144-085-3	Sequence 3, Appli
	30	166	6.3	1446	4	US-09-252-991A-5355	Sequence 5355, Ap
	31	154	5.9	44377	2	US-08-804-227C-7	Sequence 7, Appli
	32	154	5.9	44377	2	US-08-804-198-1	Sequence 1, Appli
	33	151.5	5.8	10023	4	US-09-252-991A-6997	Sequence 6997, Ap
	34	151	5.8	1896	4	US-09-107-532A-2923	Sequence 2923, Ap
c	35	149	5.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	36	149	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	37	148.5	5.7	4425	1	US-08-222-616-32	Sequence 32, Appl
	38	148.5	5.7	4425	4	US-08-446-648-32	Sequence 32, Appl
	39	148.5	5.7	4425	4	US-09-982-610-32	Sequence 32, Appl
	40	148.5	5.7	4425	5	PCT-US95-04228-32	Sequence 32, Appl
	41	144.5	5.5	71989	4	US-09-443-501A-2	Sequence 2, Appli
	42	144	5.5	2409	4	US-09-252-991A-1259	Sequence 1259, Ap
c	43	142.5	5.4	77536	4	US-09-410-551B-1	Sequence 1, Appli
	44	142	5.4	77536	4	US-09-410-551B-1	Sequence 1, Appli
c	45	140.5	5.4	2022	4	US-09-252-991A-8890	Sequence 8890, Ap

ALIGNMENTS

RESULT 1

US-09-385-028-16

; Sequence 16, Application US/09385028

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 4, 2004, 17:14:45 ; Search time 784 Seconds
(without alignments)
2979.263 Million cell updates/sec

Title: US-09-743-209A-2
Perfect score: 2618
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09743209/runat_02062004_111814_22028/app_query.fasta_1
.711

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09743209 @CGN_1_1_912 @runat_02062004_111814_22028
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	2618	100.0	1542	16	US-10-458-201-16✓	Sequence 16, Appl
	2	2618	100.0	11604	16	US-10-458-201-13✓	Sequence 13, Appl
	3	2618	100.0	15120	16	US-10-458-201-1✓	Sequence 1, Appli
c	4	420.5	16.1	32329	13	US-10-374-903A-1	Sequence 1, Appli
	5	281.5	10.8	2120	13	US-10-425-114-25288	Sequence 25288, A
	6	278.5	10.6	2132	13	US-10-425-114-35023	Sequence 35023, A
	7	274	10.5	1956	13	US-10-282-122A-26161	Sequence 26161, A
c	8	273.5	10.4	40138	15	US-10-331-061-12	Sequence 12, Appl
	9	271	10.4	1959	13	US-10-282-122A-28486	Sequence 28486, A
	10	269	10.3	1971	13	US-10-425-114-21636	Sequence 21636, A
	11	269	10.3	1990	13	US-10-425-114-22644	Sequence 22644, A
	12	265.5	10.1	1770	13	US-10-282-122A-30298	Sequence 30298, A
	13	259.5	9.9	2080	13	US-10-425-114-13515	Sequence 13515, A
	14	259.5	9.9	2080	13	US-10-425-114-17231	Sequence 17231, A
	15	259.5	9.9	2115	13	US-10-425-114-33954	Sequence 33954, A
	16	259.5	9.9	2162	13	US-10-425-114-29113	Sequence 29113, A
	17	259.5	9.9	2178	13	US-10-425-114-22140	Sequence 22140, A
	18	258	9.9	1929	13	US-10-282-122A-25744	Sequence 25744, A
	19	257.5	9.8	1866	13	US-10-282-122A-14193	Sequence 14193, A
	20	251.5	9.6	1863	15	US-10-166-087-3	Sequence 3, Appli
c	21	251.5	9.6	32539	15	US-10-166-087-1	Sequence 1, Appli
	22	245	9.4	2121	13	US-10-425-114-24843	Sequence 24843, A
	23	245	9.4	2199	13	US-10-425-114-28820	Sequence 28820, A
	24	245	9.4	2228	13	US-10-425-114-29114	Sequence 29114, A
	25	245	9.4	2248	13	US-10-425-114-1380	Sequence 1380, Ap
	26	244	9.3	2155	13	US-10-425-114-28232	Sequence 28232, A
	27	244	9.3	2159	13	US-10-425-114-24881	Sequence 24881, A
	28	244	9.3	2168	13	US-10-425-114-28007	Sequence 28007, A
	29	244	9.3	2172	13	US-10-425-114-26770	Sequence 26770, A
	30	244	9.3	2175	13	US-10-425-114-24463	Sequence 24463, A
	31	244	9.3	2175	13	US-10-425-114-24505	Sequence 24505, A
	32	244	9.3	2181	13	US-10-425-114-24584	Sequence 24584, A
	33	244	9.3	2182	13	US-10-425-114-28805	Sequence 28805, A
	34	237	9.1	1803	13	US-10-282-122A-25625	Sequence 25625, A
	35	237	9.1	1962	13	US-10-282-122A-11420	Sequence 11420, A
	36	233	8.9	1665	13	US-10-282-122A-39542	Sequence 39542, A
c	37	232.5	8.9	85692	17	US-10-461-194-1	Sequence 1, Appli
	38	232	8.9	1665	13	US-10-282-122A-20291	Sequence 20291, A
	39	232	8.9	2183	13	US-10-424-599-54780	Sequence 54780, A

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 4, 2004, 20:42:00 ; Search time 4976 Seconds
(without alignments)
3072.636 Million cell updates/sec

Title: US-09-743-209A-2
Perfect score: 2618
Sequence: 1 GAPVLPAAFGFLASARTGGG.....EVDTDVVRSVADRTARGAA 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US09743209/runat_02062004_111815_22122/app_query.fasta_1
.711
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09743209 @CGN_1_1_6425 @runat_02062004_111815_22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				Description
			Match	Length	DB	ID	
No.	Score						
1	259.5	9.9	2209	11	AY103777	AY103777	Zea mays
2	215.5	8.2	2368	28	BH770685	BH770685	LLMGtag43
3	192.5	7.4	1124	14	CK161710	CK161710	FGAS01428
4	187	7.1	4268	11	BC050123	BC050123	Mus muscu
5	183.5	7.0	710	13	CA131061	CA131061	SCBFRT106
6	183	7.0	1948	11	AK076207	AK076207	Mus muscu
7	182.5	7.0	792	14	CF554479	CF554479	GgW63 Inf
8	179.5	6.9	785	14	CB643864	CB643864	OSJNEb04M
9	177.5	6.8	783	14	CF642951	CF642951	D58_A05 F
10	176	6.7	938	14	CK268111	CK268111	EST714189
11	175.5	6.7	949	14	CK261193	CK261193	EST707271
12	175.5	6.7	1098	14	CK162420	CK162420	FGAS01501
c 13	173.5	6.6	691	14	CF035102	CF035102	QCG14a05.
14	171.5	6.6	686	14	CA266264	CA266264	SCAGLB204
15	171	6.5	624	13	CA137709	CA137709	SCCCRT200
16	170.5	6.5	886	14	CK271149	CK271149	EST717227
17	169.5	6.5	908	12	BM816283	BM816283	HB105G02_
18	166.5	6.4	849	12	BG583158	BG583158	EST484908
19	166.5	6.4	955	14	CK274379	CK274379	EST720457
20	166	6.3	921	29	CG346285	CG346285	OG0CO72TV
c 21	165.5	6.3	694	14	CF036180	CF036180	QCG28f07.
22	164.5	6.3	1041	13	C23701	C23701	C23701 Dict
23	164.5	6.3	3547	11	BC030024	BC030024	Homo sapi
24	164	6.3	975	14	CK263078	CK263078	EST709156
25	163.5	6.2	834	12	BG582349	BG582349	EST484092
26	163.5	6.2	880	14	CK270713	CK270713	EST716791
27	162.5	6.2	627	14	CF645006	CF645006	K28_A02 F
28	162.5	6.2	667	14	CF644832	CF644832	K26_A02 F
29	162	6.2	793	14	CF554543	CF554543	GgW127 In